

**APPENDIX B**  
**CURRENTLY PENDING CLAIMS**

1. (amended) A system comprising  
an isolated nucleic acid having a length of at least 5 base pairs and having  
a nucleotide sequence that comprises a first protein binding site and a second protein  
binding site where said first and second protein binding sites are spaced in proximity to  
each other such that:

when said first protein binding site is specifically bound by a protein, said  
second binding site cannot be bound by a protein that otherwise specifically recognizes  
and binds said second binding site; and

when said second binding site is specifically bound by a protein, said first  
binding site cannot be bound by a protein that otherwise specifically recognizes and binds  
said first binding site; and

a nucleic acid binding protein that specifically binds said first protein  
binding site or said second protein binding site.

2. (amended) The system of claim 1, wherein said nucleic acid is a  
double-stranded nucleic acid.

3. (amended) The system of claim 1, wherein said nucleic acid is a  
deoxyribonucleic acid (DNA).

4. (amended) The system of claim 1, wherein said first binding site  
and said second binding site have the same nucleotide sequence.

5. (amended) The system of claim 1, wherein said first binding site  
and said second binding site have the nucleotide sequence of SEQ ID NO: 1.

6. (amended) The system of claim 1, wherein said first binding site or said second binding site is specifically recognized and bound by a protein selected from the group consisting of Fis, and Tus.

7. (amended) The system of claim 1, wherein said first binding site or said second binding site is bound by EF-tu.

8. (amended) The system of claim 1, wherein said first binding site is within 20 nucleotides of said second binding site.

9. (amended) The system of claim 1, wherein said first binding site is within 11 nucleotides of said second binding site.

10. (amended) The system of claim 8, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

11. (amended) The system of claim 1, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

12. (drawn to a non-elected species) The composition of claim 1, further comprising a third protein binding site wherein said third site is in proximity to said first protein binding site or to said second protein binding site such that specific binding of said third binding site with a protein precludes specific protein binding of said first or said second protein binding sites.

13. (amended) T The system of claim 1, wherein:  
said first protein binding site is a Fis binding site;  
said second protein binding site is a Fis binding site; and

said binding sites are separated from each other by less than 12 nucleotide base pairs.

14. (amended) The system of claim 13, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

15. (amended) A composition comprising, an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that comprises a first protein binding site, a second protein binding site, and a third protein binding site where said protein binding sites are spaced in proximity to each other such that:

when either said first protein binding site or said third protein binding is specifically bound by a nucleic acid binding protein, said second binding site cannot be bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said second binding site; and

where said first protein binding site and said third protein binding site can simultaneously be specifically bound by a nucleic acid binding protein.

16. (drawn to a non-elected species) The composition of claim 15, wherein said first protein binding site or said third protein binding site is bound by a nucleic acid binding protein.

17. (drawn to a non-elected species) The composition of claim 15, wherein said third protein binding site is bound by a nucleic acid binding protein.

18. (drawn to a non-elected species) The composition of claim 17, wherein said binding protein is attached to a gene transactivator.

19. (drawn to a non-elected species) The composition of claim 18, wherein said transactivator is a Gal4 transactivator.

20. (drawn to a non-elected species) The composition of claim 15, further comprising a gene or cDNA under the control of said transactivator.

21. (drawn to a non-elected species) The composition of claim 20, further comprising a gene or cDNA under the control of said transactivator.

22. (drawn to a non-elected species) The composition of claim 21, wherein said gene is a reporter gene.

23. (drawn to a non-elected species) The composition of claim 21, wherein said gene encodes a nucleic acid binding protein.

24. (drawn to a non-elected species) The composition of claim 15, wherein said nucleic acid is a double-stranded nucleic acid.

25. (drawn to a non-elected species) The composition of claim 15, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

26. (drawn to a non-elected species) The composition of claim 15, wherein said first binding site and said third binding site have the same nucleotide sequence.

27. (drawn to a non-elected species) The composition of claim 15, wherein said first binding site or said second binding Site is specifically recognized and bound by a protein selected from the group consisting of Fis, and Tus.

28. (drawn to a non-elected species) The composition of claim 15, wherein said first binding site or said second binding site is bound by EF-tu.

29. (drawn to a non-elected species) The composition of claim 15, wherein said first binding site is within 20 nucleotides of said second binding site.

30. (drawn to a non-elected species) The composition of claim 15, wherein said first binding site is within 11 nucleotides of said second binding site.

31. (drawn to a non-elected species) The composition of claim 30, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

32. (drawn to a non-elected species) The composition of claim 15, wherein the difference in strength between said first protein binding site and said second protein binding site is at least 0 bits as determined by individual information theory.

33. The composition of claim 1, wherein:  
said first protein binding site is a Fis binding site;  
said third protein binding site is a Fis binding site.

34. (amended) A composition for the storage of binary information, said composition comprising an isolated nucleic acid having a length of at least 3 base pairs and having a nucleotide sequence that encodes a first protein binding site and a second protein binding site where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a protein, said second binding site cannot be bound by a protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a protein, said first binding site cannot be bound by a protein that otherwise specifically recognizes and binds said first binding site; and

further comprising a nucleic acid binding protein bound to said first protein binding site or said second protein binding site.

35. The composition of claim 34, wherein said nucleic acid is a double-stranded nucleic acid.

36. The composition of claim 34, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

37. The composition of claim 34, wherein said first binding site and said second binding site have the same nucleotide sequence.

38. The composition of claim 34, wherein said first binding site or said second binding site is specifically recognized and bound by a protein selected from the group consisting of Fis, and Tus.

39. The composition of claim 34, wherein said first binding site is within 20 nucleotides of said second binding site.

40. The composition of claim 34, wherein said first binding site is within 20 nucleotides of said second binding site.

41. The composition of claim 40, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

42. (amended) The composition of claim 34, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

43. (drawn to a non-elected species) The composition of claim 34, further comprising a third protein binding site wherein said third site is in proximity said first protein binding site or said second protein binding site such that specific binding of

said third binding site with a protein precludes specific protein binding of said first or said second protein binding sites.

44. The composition of claim 34, wherein:  
said first protein binding site is a Fis binding site;  
said second protein binding site is a Fis binding site;  
and said binding sites are separated from each other by less than 12 nucleotide base pairs.

45. The composition of claim 44, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

46. The composition of claim 34, wherein said binding protein is attached to a gene transactivator.

47. The composition of claim 46, wherein said transactivator is a Gal4 transactivator.

48. The composition of claim 46, further comprising a gene or cDNA under the control of said transactivator.

49. The composition of claim 48, wherein said gene is a reporter gene.

50. The composition of claim 48, wherein said gene encodes a nucleic acid binding protein.

51. (amended) A method of storing information, said method comprising the step of:

binding a nucleic acid binding protein to a first protein binding site on a nucleic acid, wherein said nucleic acid has a length of at least 3 base pairs and said nucleic acid comprises [encodes] said first protein binding site and a second protein binding site where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a protein, said second binding site cannot be bound by a protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a protein, said first binding site cannot be bound by a protein that otherwise specifically recognizes and binds said first binding site.

52. The method of claim 51, further comprising the step of determining which binding site on said nucleic acid is bound by said binding protein.

53. The method of claim 51, wherein said nucleic acid is a double-stranded nucleic acid.

54. The method of claim 51, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

55. The method of claim 51, wherein said first binding site and said second binding site have the same nucleotide sequence.

56. The method of claim 55, wherein said first binding site and said second binding site have the nucleotide sequence of SEQ ID NO: 1.



57. The method of claim 51, wherein said first binding site or said second binding site is specifically recognized and bound by a protein selected from the group consisting of Fis, EF-tu, and Tus.

58. The method of claim 51, wherein said first binding site is within 20 nucleotides of said second binding site.

59. The method of claim 51, wherein said first binding site is within 11 nucleotides of said second binding site.

60. The method of claim 51, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

61. (amended) The method of claim 51, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

62. The method of claim 51, wherein:  
said first protein binding site is a Fis binding site;  
said second protein binding site is a Fis binding site; and  
said binding sites are separated from each other by less than 12 nucleotide base pairs.

63. (amended) The system of claim 13, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

64. (drawn to a non-elected species) A method of transforming binary information, said method comprising the steps of:

(i) binding a nucleic acid binding protein to an input protein binding site on a first nucleic acid; and

(ii) determining whether or not a nucleic acid binding protein can bind to an output protein binding site on a second nucleic acid;

wherein said first nucleic acid is an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that encodes a first protein binding site, a second protein binding site, and a third protein binding site where said protein binding sites are spaced in proximity to each other such that:

when either said first protein binding site or said third protein binding is specifically bound by a nucleic acid binding protein, said second binding site cannot be bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said second binding site; and

where said first protein binding site and said third protein binding site can simultaneously be specifically bound by a nucleic acid binding protein.

65. (drawn to a non-elected species) The method of claim 64, wherein said first nucleic acid and said second nucleic acid are the same nucleic acid.